

09/831452

JC08 Rec'd PCT/PTO 10 MAY 2001

## SEQUENCE LISTING

&lt;110&gt; Japan Science and Technology Corporation

&lt;120&gt; Protein AMSH and cDNA thereof

&lt;130&gt; 99-F-054PCT/YS

5 &lt;140&gt; PCT/JP99/06309

&lt;141&gt; 1999-11-12

&lt;150&gt; JP No. 10-322674

&lt;151&gt; 1998-11-12

&lt;160&gt; 4

10 &lt;170&gt; PatentIn Ver. 2.0

&lt;210&gt; 1

&lt;211&gt; 424

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

15 &lt;400&gt; 1

Met Ser Asp His Gly Asp Val Ser Leu Pro Pro Glu Asp Arg Val Arg

1 5 10 15

Ala Leu Ser Gln Leu Gly Ser Ala Val Glu Val Asn Glu Asp Ile Pro

20 25 30

20 Pro Arg Arg Tyr Phe Arg Ser Gly Val Glu Ile Ile Arg Met Ala Ser

35 40 45

Ile Tyr Ser Glu Glu Gly Asn Ile Glu His Ala Phe Ile Leu Tyr Asn

50 55 60

Lys Tyr Ile Thr Leu Phe Ile Glu Lys Leu Pro Lys His Arg Asp Tyr

25 65 70 75 80

Lys Ser Ala Val Ile Pro Glu Lys Lys Asp Thr Val Lys Lys Leu Lys

85 90 95

Glu Ile Ala Phe Pro Lys Ala Glu Glu Leu Lys Ala Glu Leu Leu Lys

100                    105                    110  
Arg Tyr Thr Lys Glu Tyr Thr Glu Tyr Asn Glu Glu Lys Lys Lys Glu  
115                    120                    125  
Ala Glu Glu Leu Ala Arg Asn Met Ala Ile Gln Gln Glu Leu Glu Lys  
5        130                    135                    140  
Glu Lys Gln Arg Val Ala Gln Gln Lys Gln Gln Gln Leu Glu Gln Glu  
145                    150                    155                    160  
Gln Phe His Ala Phe Glu Glu Met Ile Arg Asn Gln Glu Leu Glu Lys  
165                    170                    175  
10      Glu Arg Leu Lys Ile Val Gln Glu Phe Gly Lys Val Asp Pro Gly Leu  
180                    185                    190  
Gly Gly Pro Leu Val Pro Asp Leu Glu Lys Pro Ser Leu Asp Val Phe  
195                    200                    205  
Pro Thr Leu Thr Val Ser Ser Ile Gln Pro Ser Asp Cys His Thr Thr  
15        210                    215                    220  
Val Arg Pro Ala Lys Pro Pro Val Val Asp Arg Ser Leu Lys Pro Gly  
225                    230                    235                    240  
Ala Leu Ser Asn Ser Glu Ser Ile Pro Thr Ile Asp Gly Leu Arg His  
245                    250                    255  
20      Val Val Val Pro Gly Arg Leu Cys Pro Gln Phe Leu Gln Leu Ala Ser  
260                    265                    270  
Ala Asn Thr Ala Arg Gly Val Glu Thr Cys Gly Ile Leu Cys Gly Lys  
275                    280                    285  
Leu Met Arg Asn Glu Phe Thr Ile Thr His Val Leu Ile Pro Lys Gln  
25        290                    295                    300  
Ser Ala Gly Ser Asp Tyr Cys Asn Thr Glu Asn Glu Glu Leu Phe  
305                    310                    315                    320  
Leu Ile Gln Asp Gln Gln Gly Leu Ile Thr Leu Gly Trp Ile His Thr

325                    330                    335  
His Pro Thr Gln Thr Ala Phe Leu Ser Ser Val Asp Leu His Thr His  
340                    345                    350  
Cys Ser Tyr Gln Met Met Leu Pro Glu Ser Val Ala Ile Val Cys Ser  
5                        355                    360                    365  
Pro Lys Phe Gln Glu Thr Gly Phe Phe Lys Leu Thr Asp His Gly Leu  
370                    375                    380  
Glu Glu Ile Ser Ser Cys Arg Gln Lys Gly Phe His Pro His Ser Lys  
385                    390                    395                    400  
10    Asp Pro Pro Leu Phe Cys Ser Cys Ser His Val Thr Val Val Asp Arg  
        405                    410                    415  
Ala Val Thr Ile Thr Asp Leu Arg  
        420

<210> 2  
15    <211> 1910  
<212> DNA  
<213> Homo sapiens  
<221> CDS  
<222> 11.. 1282  
20    <400> 2

cttggtcctg atgtctgacc atggagatgt gagcctcccg cccgaagacc gggtgagggc 60  
tctctccag ctggtagtg cgtagaggt gaatgaagac attccacccc gtcggtaactt 120  
ccgctctgga gttgagatta tccgaatggc atccatttac tctgaggaag gcaacattga 180  
acatgccttc atcctctata acaagtatac cacgccttt attgagaaac tacaaaaca 240  
25    tcgagattac aaatctgctg tcattcctga aaagaaagac acagtaaaga aattaaagga 300  
gattgcattt cccaaagcag aagagctgaa ggcagagctg ttaaaaacgat ataccaaaga 360  
atatacagaa tataatgaag aaaagaagaa ggaagcagag gaattggccc ggaacatggc 420  
catccagcaa gagctggaaa agaaaaaca gaggtagca caacagaagc agcagcaatt 480

ggaacaggaa cagttccatg cttcgagga gatgatccgg aaccaggagc tagaaaaaga 540  
gcgactgaaa attgtacagg agtttggaa ggttagccct ggcctaggtg gcccgtagt 600  
gcctgacttg gagaagccct ccttagatgt gttccccacc ttaacagtct catccataca 660  
gccttcagac tgtcacacaa ctgttaaggcc agctaagcca cctgtggtgg acaggtcctt 720  
5 gaaacctgga gcactgagca actcagaaaag tattccaca atcgatggat tgcccatgt 780  
ggtgtgcct gggcggctgt gcccacagtt tctccagttt gccagtgccca acactgccc 840  
gggagtgagg acatgtggaa ttctctgtgg aaaactgtatg aggaatgaat ttaccattac 900  
ccatgttctc atccccaaagc aaagtgcgtt gtctgattac tgcaacacag agaacgaaga 960  
agaacttttc ctcatcagg atcagcaggc cctcatcaca ctgggctgga ttcatactca 1020  
10 ccccacacag accgcgttcc tctccagttgt cgacccatcac actcactgtt cttaccagat 1080  
gtatgtgcctt gagtcagtag ccattgttttgc tcccccaag ttccaggaaa ctggattctt 1140  
taaactaact gaccatggac tagaggagat ttcttcgtt cggccagaaag gatttcatcc 1200  
acacagcaag gatccacccctc tggtctgttag ctgcagccac gtgactgttg tggacagagc 1260  
agtgaccatc acagacccctc gatgagcgtt tgagtccaaac accttccaaag aacaacaaaa 1320  
15 ccatatcagt gtactgttagc cccttaattt aagctttcta gaaagcttttgc gaagtttttgc 1380  
tagatagtag aaaggggggc atcacctgag aaagagctga ttttgtatattt caggtttgaa 1440  
aagaataac tgaacatatt ttttaggcaa gtcagaaaga gaacatggtc accccaaaagc 1500  
aactgtact cagaaattaa gttactcaga aattaatgtt ctcagaaattt aagaatgtt 1560  
ggtataatgtt accccatat acccttcctt ctggattcac caattgtttaa catttttttc 1620  
20 ctctcagcta tccttctaat ttctctctaa ttcaatttttgc ttatatttta cctctggct 1680  
caataagggc atctgtgcag aaatttggaa gccattttaga aaatcttttgc gatttcgtt 1740  
tggtttatgg caatatgtt ggagcttattt actgggggtga gggacagctt actccatttgc 1800  
accagattgtt ttggcttaca catcccgaag aatgattttgc tcaggtttaa ttgttatttgc 1860  
ataaatattt caggatattt ttctctaca ataaatgtt aatgtt 1910  
25 <210> 3  
<211> 424  
<212> PRT  
<213> mouse

&lt;400&gt; 3

Met Ser Asp His Gly Asp Val Ser Leu Pro Pro Gln Asp Arg Val Arg  
1 5 10 15  
Ile Leu Ser Gln Leu Gly Ser Ala Val Glu Leu Asn Glu Asp Ile Pro  
5 20 25 30  
Pro Arg Arg Tyr Tyr Arg Ser Gly Val Glu Ile Ile Arg Met Ala Ser  
35 40 45  
Val Tyr Ser Glu Glu Gly Asn Ile Glu His Ala Phe Ile Leu Tyr Asn  
50 55 60  
10 Lys Tyr Ile Thr Leu Phe Ile Glu Lys Leu Pro Lys His Arg Asp Tyr  
65 70 75 80  
Lys Ser Ala Ile Ile Pro Glu Lys Lys Asp Ala Val Lys Lys Leu Lys  
85 90 95  
Ser Val Ala Phe Pro Lys Ala Glu Glu Leu Lys Thr Glu Leu Leu Arg  
15 100 105 110  
Arg Tyr Thr Lys Glu Tyr Glu Gln Tyr Lys Glu Arg Lys Lys Glu  
115 120 125  
Glu Glu Glu Leu Ala Arg Asn Ile Ala Ile Gln Gln Glu Leu Glu Lys  
130 135 140  
20 Glu Lys Gln Arg Val Ala Gln Gln Lys Gln Lys Gln Leu Glu Gln Glu  
145 150 155 160  
Gln Phe His Ala Phe Glu Glu Met Ile Gln Arg Gln Glu Leu Glu Lys  
165 170 175  
Glu Arg Leu Lys Ile Val Gln Glu Phe Gly Lys Val Asp Pro Gly Pro  
25 180 185 190  
Cys Gly Pro Leu Leu Pro Asp Leu Glu Lys Pro Cys Val Asp Val Ala  
195 200 205  
Pro Ser Ser Pro Phe Ser Pro Thr Gln Thr Pro Asp Cys Asn Thr Gly

210                    215                    220  
Met Arg Pro Ala Lys Pro Pro Val Val Asp Arg Ser Leu Lys Pro Gly  
225                    230                    235                    240  
Ala Leu Ser Val Ile Glu Asn Val Pro Thr Ile Glu Gly Leu Arg His  
5                      245                    250                    255  
Ile Val Val Pro Arg Asn Leu Cys Ser Glu Phe Leu Gln Leu Ala Ser  
                    260                      265                    270  
Ala Asn Thr Ala Lys Gly Ile Glu Thr Cys Gly Val Leu Cys Gly Lys  
                    275                      280                    285  
10   Leu Met Arg Asn Glu Phe Thr Ile Thr His Val Leu Ile Pro Arg Gln  
                    290                      295                    300  
Asn Gly Gly Pro Asp Tyr Cys His Thr Glu Asn Glu Glu Glu Ile Phe  
                    305                      310                    315                    320  
Phe Met Gln Asp Asp Leu Gly Leu Leu Thr Leu Gly Trp Ile His Thr  
15                      325                    330                    335  
His Pro Thr Gln Thr Ala Phe Leu Ser Ser Val Asp Leu His Thr His  
                    340                      345                    350  
Cys Ser Tyr Gln Met Met Leu Pro Glu Ser Ile Ala Ile Val Cys Ser  
                    355                      360                    365  
20   Pro Lys Phe Gln Glu Thr Gly Phe Phe Lys Leu Thr Asp Tyr Gly Leu  
                    370                      375                    380  
Gln Glu Ile Ser Thr Cys Arg Gln Lys Gly Phe His Pro His Gly Arg  
                    385                      390                    395                    400  
Asp Pro Pro Leu Phe Cys Asp Cys Ser His Val Thr Val Lys Asp Arg  
25                      405                    410                    415  
Ile Val Thr Ile Thr Asp Leu Arg  
                    420

<211> 1384

<212> DNA

<213> homosapiens

<221> CDS

5 <222> 56..1327

<400> 4

gtgacgtttc cggaagctct gactgtcatc cttcacgaaa gaaccttattt gtccaatgtc 60

tgaccatggg gatgtgagcc tcccacccca agacccggtg aggattctgt cccaaacttgg 120

gagtgcagtt gagttaaatg aagacattcc accccgtcgc tactaccgct ccggtgttga 180

10 gatcatccgc atggcgtccg tttactcgga agaaggcaac attgaacatg cctttatcct 240

ctacaacaag tacatcacgc tgtttatttga aaaacttccg aaacaccgag actacaaatc 300

agctatcatt cctgagaaga aagatgctgt caagaatta aagagcgtcg ctttcctaa 360

agcggaaagag ctgaagacag agctctttag aagatacacc aaagaatatg agcagtataa 420

agagcgaagaaaaaaggaag aagaggaact tgcccgaat atcgccatcc agcaagagtt 480

15 ggaaaaagaa aaacagaggg ttgctcagca gaagcagaag cagctagagc aggagcaatt 540

ccatgccttt gaggagatga tccagaggca ggagctggaa aaagaacggc tgaaaattgt 600

tcaagagttc gggaaaggtag accctggccc ctgcgggcct ctgctccctg atctggaaaa 660

gccttgcgtta gatgtggccc ccagctcacc gttctcgccc acgcagactc cagactgtaa 720

cacaggcatg aggccagcta agccacctgt ggtggacagg tccctgaaac ctggagcggtt 780

20 aagcgtcata gaaaatgttc ccaccattga aggcctgcgc cacatcggtt tgccccgtaa 840

tctgtgcgtca gaatttctcc agcttgcag tgccaatacc gccaaaggca ttgaaacctg 900

tggagtccctc tgtggaaaac tggatgagaaa tgaattcaca atcacacatg ttctcatccc 960

cagacaaaat ggtggccctg attattgcca cacggagaat gaagaagaaa ttttctttat 1020

gcaggatgac ctggactcc tcactcttgg ctggatccat actcatccaa cccaaacggc 1080

25 ctttctgtcc agtgtggatc tccacactca ctgctccctac caaatgtatgt taccagagtc 1140

catcgcaatc gtctgttccc caaagttcca ggaaactgga ttctttaagc taactgacta 1200

tggtcttcaa gagatttcaa cctgccggca gaaaggcttt caccccccattt gcagagaccc 1260

accgctgttc tgtgactgca gccatgtcac tgtcaaggac agaattgtga cgatcacaga 1320

090331452 , 061001

8/8

ccttcgataa atctcaaatc atgaaccagg gagatggatc actggtaac agcacttgtc 1380

acca

1384